



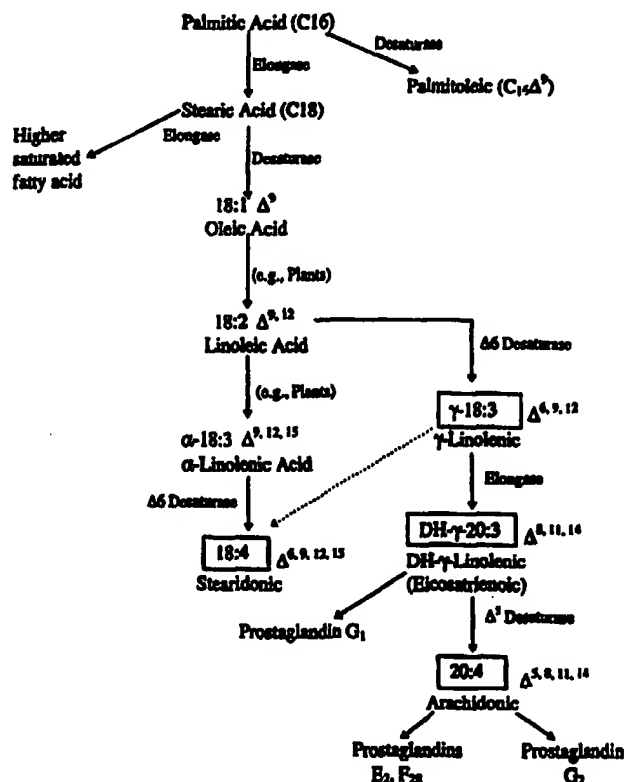
## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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|--|-----------|---|
| <b>(51) International Patent Classification <sup>6</sup> :</b><br><br>C12N 15/53, 15/81, 9/02, 5/10, 1/19,<br>C12P 7/64, C11B 1/00, A61K 31/20,<br>A23L 1/30   | <b>A1</b> | <b>(11) International Publication Number:</b> WO 98/46763<br><br><b>(43) International Publication Date:</b> 22 October 1998 (22.10.98)   |
| <b>(21) International Application Number:</b> PCT/US98/07126<br><br><b>(22) International Filing Date:</b> 10 April 1998 (10.04.98)<br><br><b>(30) Priority Data:</b><br>08/834,655 11 April 1997 (11.04.97) US<br><br><b>(63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application</b><br>US 08/834,655 (CIP)<br>Filed on 11 April 1997 (11.04.97)<br><br><b>(71) Applicants (for all designated States except US):</b> CALGENE LLC [US/US]; 1920 Fifth Street, Davis, CA 95616 (US). ABBOTT LABORATORIES [US/US]; 100 Abbott Park Road, Abbott Park, IL 60064-3500 (US).<br><br><b>(72) Inventors; and</b><br><b>(75) Inventors/Applicants (for US only):</b> KNUTZON, Deborah [US/US]; 6110 Rockhurst Way, Granite Bay, CA 95746 (US). MUKERJI, Pradip [US/US]; 1069 Arcaro Drive, Gahanna, OH 43230 (US). HUANG, Yung-Sheng [CA/US]; 2462 Danvers Court, Upper Arlington, OH 43220 (US). THURMOND, Jennifer [US/US]; 3702 Adirondack, Colum- |           | <b>(74) Agents:</b> WARD, Michael, R. et al.; Limbach & Limbach L.L.P., 2001 Ferry Building, San Francisco, CA 94111-4262 (US).<br><br><b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).<br><br><b>Published</b><br><i>With international search report.</i><br><i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> |

(54) Title: METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLYUNSATURATED FATTY ACIDS

## (57) Abstract

The present invention relates to fatty acid desaturases able to catalyze the conversion of oleic acid to linoleic acid, linoleic acid to  $\gamma$ -linolenic acid, or of  $\alpha$ -linolenic acid to stearidonic acid. Nucleic acid sequences encoding desaturases, nucleic acid sequences which hybridize thereto, DNA constructs comprising a desaturase gene, and recombinant host microorganism or animal expressing increased levels of a desaturase are described. Methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing increased levels of a desaturase are disclosed. Fatty acids, and oils containing them, which have been desaturated by a desaturase produced by recombinant host microorganisms or animals are provided. Pharmaceutical compositions, infant formulas or dietary supplements containing fatty acids which have been desaturated by a desaturase produced by a recombinant host microorganism or animal also are described.



The present invention is further directed to transgenic oils in pharmaceutically acceptable carriers. The present invention is further directed to nutritional supplements, cosmetic agents and infant formulae containing transgenic oils.

5           The present invention is further directed to a method for obtaining altered long chain polyunsaturated fatty acid biosynthesis comprising the steps of: growing a microbe having cells which contain a transgene which encodes a transgene expression product which desaturates a fatty acid molecule at carbon 6 or 12 from the carboxyl end of said fatty acid molecule, wherein the transgene  
10           is operably associated with an expression control sequence, under conditions whereby the transgene is expressed, whereby long chain polyunsaturated fatty acid biosynthesis in the cells is altered.

          The present invention is further directed toward pharmaceutical compositions comprising at least one nutrient selected from the group consisting  
15           of a vitamin, a mineral, a carbohydrate, a sugar, an amino acid, a free fatty acid, a phospholipid, an antioxidant, and a phenolic compound.

### **BRIEF DESCRIPTION OF THE DRAWINGS**

          Figure 1 shows possible pathways for the synthesis of arachidonic acid  
20           (20:4  $\Delta$ 5, 8, 11, 14) and stearidonic acid (18:4  $\Delta$ 6, 9, 12, 15) from palmitic acid ( $C_{16}$ ) from a variety of organisms, including algae, *Mortierella* and humans. These PUFAs can serve as precursors to other molecules important for humans and other animals, including prostacyclins, leukotrienes, and prostaglandins, some of which are shown.

25           Figure 2 shows possible pathways for production of PUFAs in addition to ARA, including EPA and DHA, again compiled from a variety of organisms.

          Figure 3A-E shows the DNA sequence of the *Mortierella alpina*  $\Delta$ 6-desaturase and the deduced amino acid sequence:

          Figure 3A-E (SEQ ID NO 1  $\Delta$ 6 DESATURASE cDNA)

Figure 3A-E (SEQ ID NO 2  $\Delta 6$  DESATURASE AMINO ACID)

Figure 4 shows an alignment of a portion of the *Mortierella alpina*  $\Delta 6$ -desaturase amino acid sequence with other related sequences.

5 Figure 5A-D shows the DNA sequence of the *Mortierella alpina*  $\Delta 12$ -desaturase and the deduced amino acid sequence:

Figure 5A-D (SEQ ID NO 3  $\Delta 12$  DESATURASE cDNA)

Figure 5A-D (SEQ ID NO 4  $\Delta 12$  DESATURASE AMINO ACID).

Figures 6A and 6B show the effect of different expression constructs on expression of GLA in yeast.

10 Figures 7A and 7B show the effect of host strain on GLA production.

Figures 8A and 8B show the effect of temperature on GLA production in *S. cerevisiae* strain SC334.

Figure 9 shows alignments of the protein sequence of the Ma 29 and contig 253538a.

15 Figure 10 shows alignments of the protein sequence of Ma 524 and contig 253538a.

#### **BRIEF DESCRIPTION OF THE SEQUENCE LISTINGS**

SEQ ID NO:1 shows the DNA sequence of the *Mortierella alpina*  $\Delta 6$ -desaturase.

20 SEQ ID NO:2 shows the protein sequence of the *Mortierella alpina*  $\Delta 6$ -desaturase.

SEQ ID NO:3 shows the DNA sequence of the *Mortierella alpina*  $\Delta 12$ -desaturase.

25 SEQ ID NO:4 shows the protein sequence of the *Mortierella alpina*  $\Delta 12$ -desaturase.

SEQ ID NO:5-11 show various desaturase sequences.

SEQ ID NO:13-18 show various PCR primer sequences.

SEQ ID NO:19 and SEQ ID NO:20 show the nucleotide and amino acid sequence of a *Dictyostelium discoideum* desaturase.

5 SEQ ID NO:21 and SEQ ID NO:22 show the nucleotide and amino acid sequence of a *Phaeodactylum tricornutum* desaturase.

SEQ ID NO:23-26 show the nucleotide and deduced amino acid sequence of a *Schizochytrium* cDNA clone.

SEQ ID NO: 27-33 show nucleotide sequences for human desaturases.

10 SEQ ID NO:34 - SEQ ID NO:40 show peptide sequences for human desaturases.

### **DESCRIPTION OF THE PREFERRED EMBODIMENTS**

In order to ensure a complete understanding of the invention, the following definitions are provided:

15  **$\Delta$ 5-Desaturase:**  $\Delta$ 5 desaturase is an enzyme which introduces a double bond between carbons 5 and 6 from the carboxyl end of a fatty acid molecule.

**$\Delta$ 6-Desaturase:**  $\Delta$ 6-desaturase is an enzyme which introduces a double bond between carbons 6 and 7 from the carboxyl end of a fatty acid molecule.

**$\Delta$ 9-Desaturase:**  $\Delta$ 9-desaturase is an enzyme which introduces a double bond between carbons 9 and 10 from the carboxyl end of a fatty acid molecule.

20  **$\Delta$ 12-Desaturase:**  $\Delta$ 12-desaturase is an enzyme which introduces a double bond between carbons 12 and 13 from the carboxyl end of a fatty acid molecule.

25 **Fatty Acids:** Fatty acids are a class of compounds containing a long hydrocarbon chain and a terminal carboxylate group. Fatty acids include the following:

| Fatty Acid |               |  |
|------------|---------------|--|
| 12:0       | lauric acid   |  |
| 16:0       | palmitic acid |  |

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FIG. 3A

60 \*  
 CGACACTCCT TCCTTCTTCT CACCCGTCCT AGTCCCTCTC AACCCCTCTC TTGACAAAG  
 ACAACAAACC ATG GCT GCT CCC AGT GTG AGG ACG TTT ACT CGG GCC GAG  
 Met Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu  
 120 \*  
 GTT TTG AAT GCC GAG GCT CTG AAT GAG GGC AAG AAG GAT GCC GAG GCA  
 Val Leu Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala  
 180 \*  
 CCC TTC TTG ATG ATC GAC AAC AAG GTG TAC GAT GTC CGC GAG TTC  
 Pro Phe Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe  
 240 \*  
 GTC CCT GAT CAT CCC GGT GGA AGT GTG ATT CTC ACG CAC GTT GGC AAG  
 Val Pro Asp His Pro Gly Ser Val Ile Leu Thr His Val Gly Lys  
 300 \*  
 GAC GGC ACT GAC GTC TTT GAC ACT TTT CAC CCC GAG GCT GCT TGG GAG  
 Asp Gly Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu  
 ACT CTT GCC AAC TTT TAC GTT GGT GAT ATT GAC GAG AGC GAC CGC GAT  
 Thr Leu Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp  
 360 \*  
 ATC AAG AAT GAT GAC TTT GCG GCC GAG GTC CGC AAG CTG CGT ACC TTG  
 Ile Lys Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu

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FIG. 3B

420 \*  
 TTC CAG TCT CTT GGT TAC TAC GAT TCT TCC AAG GCA TAC TAC GCC TTC  
 Phe Gln Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe 126  
 480 \*  
 AAG GTC TCG TTC AAC CTC TGC ATC TGG GGT TTG TCG ACG GTC ATT GTG  
 Lys Val Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val 156  
 540 \*  
 GCC AAG TGG GGC CAG ACC TCG ACC CTC GCC AAC GTG CTC TCG GCT GCG  
 Ala Lys Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala 186  
 CTT TTG GGT CTG TTC TGG CAG CAG TGC GGA TGG TTG GCT CAC GAC TTT  
 Leu Leu Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe 216  
 600 \*  
 TTG CAT CAC CAG GTC TTC CAG GAC CAG CCG TTC TGG GGT GAT CTT TTC GGC  
 Leu His His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly 246  
 660 \*  
 GCC TTC TTG GGA GGT GTC TGC CAG GGC TTC TCG TCC TCG TGG TGG AAG  
 Ala Phe Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys 276  
 720 \*  
 GAC AAG CAC AAC ACT CAC CAC GCC GCC CCC AAC GTC CAC GGC GAG GAT  
 Asp Lys His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp 306  
 780 \*

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FIG. 3C

CCC GAC ATT GAC ACC CAC CCT CTG TTG ACC TGG AGT GAG CAT GCG TTG  
Pro Asp Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu

GAG ATG TTC TCG GAT GTC CCA GAT GAG GAG CTG ACC CGC ATG TGG TCG  
Glu Met Phe Ser Asp Val Pro Asp Glu Glu Thr Arg Met Trp Ser

840 \*

CGT TTC ATG GTC CTG AAC CAG ACC TGG TTT TAC TTC CCC ATT CTC TCG  
Arg Phe Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser

900 \*

TTT GCC CGT CTC TCC TGG TGC CTC CAG TCC ATT CTC TTT GTG CTG CCT.  
Phe Ala Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro

960 \*

AAC GGT CAG GCC CAC AAG CCC TCG GGC GCG CGT GTG CCC ATC TCG TTG  
Asn Gly Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu

1020 \*

GTC GAG CAG CTG TCG CTT GCG ATG CAC TGG ACC TGG TAC CTC GCC ACC  
Val Glu Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr

ATG TTC CTG TTC ATC AAG GAT CCC GTC AAC ATG CTG GTG TAC TTT TTG  
Met Phe Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu

1080 \*

GTG TCG CAG GCG GTG TGC GGA AAC TTG TGG GCG ATC GTG TTC TCG CTC  
Val Ser Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu

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FIG. 3D

1140 \*  
AAC CAC AAC GGT ATG CCT GTG ATC TCG AAG GAG GAG GCG GTC GAT ATG  
Asn His Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met

1200 \*  
GAT TTC TTC ACG AAG CAG ATC ATC ACG GGT CGT GAT GTC CAC CCG GGT  
Asp Phe Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly

1260 \*  
CTA TTT GCC AAC TGG TTC ACG GGT GGA TTG AAC TAT CAG ATC GAG CAC  
Leu Phe Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His

1320 \*  
CAC TTG TTC CCT TCG ATG CCT CGC CAC AAC TTT TCA AAG ATC CAG CCT  
His Leu Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro

1380 \*  
GCT GTC GAG ACC CTG TGC AAA AAG TAC AAT GTC CGA TAC CAC ACC ACC  
Ala Val Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr

1440 \*  
GGT ATG ATC GAG GGA ACT GCA GAG GTC TTT AGC CGT CTG AAC GAG GTC  
Gly Met Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val

1440 \*  
TCC AAG GCT GCC TCC AAG ATG GGT AAG GCG CAG TAAAAAAA AAACAAGGAC  
Ser Lys Ala Ala Ser Lys Met Gly Lys Ala Gln



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FIG. 3E

1500 \*  
GTTTTTTTC GCCAGTGCCT GTGCCGTGTC CTGCTTCCCT TGTCAAGTCG AGCGTTCTG  
1560 \*  
GAAAGGATCG TTCAGTGCAG TATCATCATTT CTCCTTTTAC CCCCCGCTCA TATCTCATTC  
ATTCTCTTA TTAACAACCT TGTTCCTCCC TTCACCG

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FIG. 5A

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60 *
GTCCCTGTC GCTGTGGCA CACCCCATCC TCCCTGGCTC OCTCTGGTT TGTCTTGGC
120 *
CCACCGTCTC TCTTCCACC TCCGAGACGA CTGCAACTGT AATCAGGAAC CGACAATAC
180 *
ACGATTTCCTT TTACTCAGC ACCAACTCAA AATCTCAAC CGCAACCTT TTTCAGG ATG
Met
GCA CCT CCC AAC ACT ATC GAT GCC GGT TTG ACC CAG CGT CAT ATC AGC
Ala Pro Pro Asn Thr Ile Asp Ala Gly Leu Thr Gln Arg His Ile Ser
240 *
ACC TCG GCC CCA AAC TCG GCC AAG CCT GCC TTC GAG CGC AAC TAC CAG
Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr Gln
300 *
CTC CCC GAG TTC ACC ATC AAG GAG ATC CGA GAG TGC ATC CCT GCC CAC
Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala His
360 *
TGC TTT GAG CGC TCC GGT CTC CGT GGT CTC TGC CAC GTT GCC ATC GAT
Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile Asp
420 *
CTG ACT TGG GCG TCG CTC TTG TTC CTG GCT GCG ACC CAG ATC GAC AAG
Leu Thr Thr Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp Lys
TTT GAG AAT CCC TTG ATC CGC TAT TTG GCC TGG CCT GTT TAC TGG ATC
Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp Ile

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FIG. 5B

480 \*  
 ATG CAG GGT ATT GTC TGC ACC GGT GTC TGG GTG CTG GCT CAC GAG TGT  
 Met Gln Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu Cys

540 \*  
 GGT CAT CAG TCC TTC TCG ACC TCC AAG ACC CTC AAC AAC ACA GTT GGT  
 Gly His Gln Ser Phe Ser Thr Ser Lys Thr Leu Asn Thr Val Gly

600 \*  
 TGG ATC TTG CAC TCG ATG CTC TTG GTC CCC TAC CAC TCC TGG AGA ATC  
 Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg Ile

660 \*  
 TCG CAC TCG AAG CAC CAC AAG GCC ACT GGC CAT ATG ACC AAG GAC CAG  
 Ser His Ser Lys His His Lys Ala Thr Gly His Met Thr Lys Asp Gln

720 \*  
 GTC TTT GTG CCC AAG ACC CGC TCC CAG GTT GGC TTG CCT CCC AAG GAG  
 Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys Glu

780 \*  
 AAC GCT GCT GCT GCC GTT CAG GAG GAG GAC ATG TCC GTG CAC CTG GAT  
 Asn Ala Ala Ala Val Gln Gln Glu Glu Asp Met Ser Val His Leu Asp

840 \*  
 GAG GAG GCT CCC ATT GTG ACT TTG TTC TGG ATG GTG ATC CAG TTC TTG  
 Glu Glu Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe Leu

900 \*  
 TTC GGA TGG CCC GCG TAC CTG ATT ATG AAC GCC TCT GGC CAA GAC TAC  
 Phe Gly Trp Pro Ala Tyr Leu Ile Met Asn Ala Ser Gly Gln Asp Tyr

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FIG. 5C

900 \*  
 GGC CGC TGG ACC TCG CAC TTC CAC ACG TAC TCG CCC ATC TTT GAG CCC  
 Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu Pro  
  
 CGC AAC TTT TTC GAC ATT ATT ATC TCG GAC CTC GGT GTG TTG GCT GCC  
 Arg Asn Phe Phe Asp Ile Ile Ile Ser Asp Leu Gly Val Leu Ala Ala  
 960 \*  
 CTC GGT GCC CTG ATC TAT GGC TCC ATG CAG TTG TCG CTC TTG ACC GTC  
 Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Ser Leu Leu Thr Val  
 1020 \*  
 ACC AAG TAC TAT ATT GTC CCC TAC CTC TTT GTC AAC TTT TGG TTG GTC  
 Thr Lys Tyr Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu Val  
 1080 \*  
 CTG ATC ACC TTC TTG CAG CAC ACC GAT CCC AAG CTG CCC CAT TAC CGC  
 Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr Arg  
 1140 \*  
 GAG GGT GCC TGG AAT TTC CAG CQT GGA GCT CTT TGC ACC GTT GAC CGC  
 Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp Arg  
  
 TCG TTT GGC AAG TTC TTG GAC CAT ATG TTC CAC GGC ATT GTC CAC ACC  
 Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His Thr  
 1200 \*  
 CAT GTG GCC CAT CAC TTG TTC TCG CAA ATG CCG TTC TAC CAT GCT GAG  
 His Val Ala His His Leu Phe Ser Gln Met Pro Phe Tyr His Ala Glu

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FIG. 5D

1260 \*  
 GAA GCT ACC TAT CAT CTC AAG AAA CTG CTG GGA GAG TAC TAT GTG TAC  
 Glu Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Tyr Val Tyr  
 1320 \*  
 GAC CCA TCC CCG ATC GTC GTT GCG GTC TGG AGG TCG TTC CGT GAG TGC  
 Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu Cys  
 1380 \*  
 CGA TTC GTG GAG GAT CAG GGA GAC GTG GTC TTT TTC AAG AAG TAAAA  
 Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys  
 1440 \*  
 AAAGGACAAT GGACCACACA CAACCTTGTC TCTACAGACC TACGTATCAT GTAGCCATAC  
 CACTTCATTA AAGACATGA GCTCTAGAGG CGTGTCTATTC GGGCCCTCC

**FastA Match of ma29 and contig 253538a**

SCORES Initl: 117 Initn: 225 Opt: 256  
 Smith-Waterman score: 408; 27.0% identity in 441 aa overlap

```

      10      20      30      40      50
ma29gcg.pep  MGTDQGKT---FTWEELAAHNTKDDLLLAIRGRVYDVTKFLSRHPGGVDTL LLGAGRDVT
      |||  |||:|:|  ::  ::  |:|  :|:|:|:|  ||||  ::  ||:|:|
253538a      QGPTPRYFTWDEVAQRSCEERWLVIDRKVYNISEFTRRHPGGSRVISHYAGQDAT
      10      20      30      40      50

      60      70      80      90      100     110
ma29gcg.pep  PVFEMYHAF-GAADAIMKKYYVGTLSNELPIFPEPTVFHKTIKTRVEGYFTDRNIDPKN
      | :|  | :  |:|  :|  ||  ||  ||  ||  ::  |  | :  :
253538a      DPFVAFHINKGLVKKYMNSLLIGEL-SPEQPSF-EPTKNKELTDEFREL RATVERMGLMK
      60      70      80      90      100     110

      120     130     140     150     160     170
ma29gcg.pep  RPEIWGRYALIFGSLIASYYAQLFVPFVVERTWLQVVF-AIIMGFACAQVGLNPLHDASH
      ::  :|  :  ::  |  ::  :|  ::  :|  ::  :|  ::  :|  ||  :|
253538a      ANHVF--FLLYLLHILLDGAAWLT LWVFGTSFLPFLLCVLLSAVQAQAGWLQ-HDYGH
      120     130     140     150     160     170

      180     190     200     210     220
ma29gcg.pep  FSVTHNPTVWKILGATHDF----FNGASYLVWVYQHMLGHHPYTN IAGADPDVSTSE---
      :||  :|  | :  | :|  :|||  | :|  :|  ||  |||:  :
253538a      LSVYRKPK-WNHL--VHKFVIGHLKGASANWNNHRH-FQHHAKPNI FHKDPDVNMLHVFV
      180     190     200     210     220

      230     240     250     260     270     280
ma29gcg.pep  ----PDVRRIKPNQKWF-VNHINQHMFV--PFLYGLLAFKVRIQDINILYFVKTND AIRV
      ::  | :  ::  ||  ::|:  ||  :  | :  :|  | :  :|  :
253538a      LGEWQPIEYGKKKLKYPYNHQHEYFFLIGPPLLIPMYFYQYQI----IMTMIVHKNWVDL
      230     240     250     260     270     280

      290     300     310     320     330     340
ma29gcg.pep  NPISTWHTVMFWGGKAFFVWYRLVPLQYLP LKVL LFTVADMVSSYWLALTFQANHVV
      :|  :  ::  ||:  |  :|:  |  ||  :|:|:  ::  | :|:  :|  ||:|
253538a      ----AWAVSYI---RFFITY---IPF-YGILG-ALLFLNFIRFLESHWFWVTQMNHIV
      290     300     310     320     330

      350     360     370     380     390
ma29gcg.pep  EEVQWPLPDENGIIQKDWAAAMQVETT----QDYAHDSHLWTSITGSLNYQAVHHLFPNVS
      |:  |::  :||  :|:  :|  |::  :|  |  |  ||:|  ||||:
253538a      MEI-----DQEAY--RDWFSSQLTATCNVEQSFFND---WFS--GHLNFQIEHHLFPTMP
      340     350     360     370

      400     410     420     430     440
ma29gcg.pep  QHHYPDILAIKNTCSEYKVPYLVKDTFWQAFASHLEHLRVLGLRPKEEX
      :|:  |  :|:  |:  :|  |
253538a      RHNLHKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKKSGKLWLDAYLHKX
      380     390     400     410     420     430

```

**Figure 9**